



SEQUENCE LISTING

#57B

(1) GENERAL INFORMATION:

- (i) APPLICANT: Lee, Jong Y.
- (ii) TITLE OF INVENTION: PURIFIED HUMAN ERYTHROPOIETIN RECEPTOR
PROTEIN FRAGMENT AND ANTIBODIES DERIVED THEREFROM
- (iii) NUMBER OF SEQUENCES: 5
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Fish & Richardson P.C., P.A.
 - (B) STREET: 60 South Sixth Street, Suite 3300
 - (C) CITY: Minneapolis
 - (D) STATE: MN
 - (E) COUNTRY: USA
 - (F) ZIP: 55402
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM compatible
 - (C) OPERATING SYSTEM: DOS
 - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 09/016,159
 - (B) FILING DATE: 30-JAN-1998
- (vi) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/876,227
 - (B) FILING DATE: 16-JUN-1997
- (vi) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/734,097
 - (B) FILING DATE: 21-OCT-1996
- (vi) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/460,525
 - (B) FILING DATE: 02-JUN-1995
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Ellinger, Mark S.
 - (B) REGISTRATION NUMBER: 34,812
 - (C) REFERENCE/DOCKET NUMBER: 07004/002003
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 612/335-5070
 - (B) TELEFAX: 612/288-9696

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: synthetic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: BamH1 linker ar 5' end followed by sequence for amino acids 25 through 29 of the full length human Epor protein. Forward primer for Sequence ID No. 2."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TTGGATCC GCG CCC CCG CCT A AC
Ala Pro Pro Pro
1

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: EcoR1 linker followed by sequence complementary to coding sequence for amino acids 226 through 222 of full length human Epor protein. Reverse primer for Sequence ID No. 1.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TGAATTCGGG GTCCAGGTCG CT

22

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(vii) IMMEDIATE SOURCE:

(B) CLONE: pGEX-2T, Pharmacia (Mechanicsburg, PA)

(ix) FEATURE:
 (A) NAME/KEY: Thrombin Cleavage Site in plasmid vector pGEX-2T."

(x) PUBLICATION INFORMATION:
 (A) AUTHORS: Smith, D.B.
 Johnson, K.S.
 (B) TITLE: Single-step purification of polypeptides
 expressed in Escherichia coli as fusions with
 glutathione-S-transferase
 (D) VOLUME: 67
 (F) PAGES: 31-40
 (G) DATE: 1988

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTG GTT CCG CGT GGA T CC
 Leu Val Pro Arg Gly
 5

18

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1527 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(x) PUBLICATION INFORMATION:
 (A) AUTHORS: Winkelmann , J. C., et al.
 (C) JOURNAL: Blood
 (D) VOLUME: 76
 (E) ISSUE: 1
 (F) PAGES: 24-30
 (G) DATE: 1990

(x) PUBLICATION INFORMATION:
 (A) AUTHORS: Jones, S.S., et al.
 (C) JOURNAL: Blood
 (D) VOLUME: 76
 (E) ISSUE: 1
 (F) PAGES: 31-35
 (G) DATE: 1990

(x) PUBLICATION INFORMATION:
 (A) AUTHORS: Noguchi, C.T., et al.
 (C) JOURNAL: Blood
 (D) VOLUME: 78
 (E) ISSUE: 10
 (F) PAGES: 2548-2556
 (G) DATE: 1991

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ATG GAC CAC CTC GGG GCG TCC CTC TGG CCC CAG GTC GGC TCC CTT TGT 48
 Met Asp His Leu Gly Ala Ser Leu Trp Pro Gln Val Gly Ser Leu Cys
 1 5 10 15

CTC CTG CTC GCT GGG GCC GCC TGG GCG CCC CCG CCT AAC CTC CCG GAC 96
 Leu Leu Leu Ala Gly Ala Ala Trp Ala Pro Pro Pro Asn Leu Pro Asp
 20 25 30

CCC AAG TTC GAG AGC AAA GCG GCC TTG CTG GCG GCC CGG GGG CCC GAA 144
 Pro Lys Phe Glu Ser Lys Ala Ala Leu Leu Ala Ala Arg Gly Pro Glu

| | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|-----|
| 35 | | | | | | 40 | | | | | | 45 | | | | | | |
| GAG | CTT | CTG | TGC | TTC | ACC | GAG | CGG | TTG | GAG | GAC | TTG | GTG | TGT | TTC | TGG | | | 192 |
| Glu | Leu | Leu | Cys | Phe | Thr | Glu | Arg | Leu | Glu | Asp | Leu | Val | Cys | Phe | Trp | | | |
| | 50 | | | | | | 55 | | | | 60 | | | | | | | |
| GAG | GAA | GCG | GCG | AGC | GCT | GGG | GTG | GGC | CCG | GGC | AAC | TAC | AGC | TTC | TCC | | | 240 |
| Glu | Glu | Ala | Ala | Ser | Ala | Gly | Val | Gly | Pro | Gly | Asn | Tyr | Ser | Phe | Ser | | | |
| | 65 | | | | 70 | | | | | 75 | | | | | 80 | | | |
| TAC | CAG | CTC | GAG | GAT | GAG | CCA | TGG | AAG | CTG | TGT | CGC | CTG | CAC | CAG | GCT | | | 288 |
| Tyr | Gln | Leu | Glu | Asp | Glu | Pro | Trp | Lys | Leu | Cys | Arg | Leu | His | Gln | Ala | | | |
| | | | | 85 | | | | | 90 | | | | | 95 | | | | |
| CCC | ACG | GCT | CGT | GGT | GCG | GTG | CGC | TTC | TGG | TGT | TCG | CTG | CCT | ACA | GCC | | | 336 |
| Pro | Thr | Ala | Arg | Gly | Ala | Val | Arg | Phe | Trp | Cys | Ser | Leu | Pro | Thr | Ala | | | |
| | | | 100 | | | | | 105 | | | | | 110 | | | | | |
| GAC | ACG | TCG | AGC | TTC | GTG | CCC | CTA | GAG | TTG | CGC | GTC | ACA | GCA | GCC | TCC | | | 384 |
| Asp | Thr | Ser | Ser | Phe | Val | Pro | Leu | Glu | Leu | Arg | Val | Thr | Ala | Ala | Ser | | | |
| | | 115 | | | | | 120 | | | | | 125 | | | | | | |
| GGC | GCT | CCG | CGA | TAT | CAC | CGT | GTC | ATC | CAC | ATC | AAT | GAA | GTA | GTG | CTC | | | 432 |
| Gly | Ala | Pro | Arg | Tyr | His | Arg | Val | Ile | His | Ile | Asn | Glu | Val | Val | Leu | | | |
| | 130 | | | | | 135 | | | | | 140 | | | | | | | |
| CTA | GAC | GCC | CCC | GTG | GGG | CTG | GTG | GCG | CGG | TTG | GCT | GAC | GAG | AGC | GGC | | | 480 |
| Leu | Asp | Ala | Pro | Val | Gly | Leu | Val | Ala | Arg | Leu | Ala | Asp | Glu | Ser | Gly | | | |
| | 145 | | | | 150 | | | | | 155 | | | | | 160 | | | |
| CAC | GTA | GTG | TTG | CGC | TGG | CTC | CCG | CCG | CCT | GAG | ACA | CCC | ATG | ACG | TCT | | | 528 |
| His | Val | Val | Leu | Arg | Trp | Leu | Pro | Pro | Pro | Glu | Thr | Pro | Met | Thr | Ser | | | |
| | | | | 165 | | | | | 170 | | | | | 175 | | | | |
| CAC | ATC | CGC | TAC | GAG | GTG | GAC | GTC | TCG | GCC | GGC | AAC | GGC | GCA | GGG | AGC | | | 576 |
| His | Ile | Arg | Tyr | Glu | Val | Asp | Val | Ser | Ala | Gly | Asn | Gly | Ala | Gly | Ser | | | |
| | | | 180 | | | | | 185 | | | | | 190 | | | | | |
| GTA | CAG | AGG | GTG | GAG | ATC | CTG | GAG | GGC | CGC | ACC | GAG | TGT | GTG | CTG | AGC | | | 624 |
| Val | Gln | Arg | Val | Glu | Ile | Leu | Glu | Gly | Arg | Thr | Glu | Cys | Val | Leu | Ser | | | |
| | 195 | | | | | 200 | | | | | | 205 | | | | | | |
| AAC | CTG | CGG | GGC | CGG | ACG | CGC | TAC | ACC | TTC | GCC | GTC | CTC | GCG | CGT | ATG | | | 672 |
| Asn | Leu | Arg | Gly | Arg | Thr | Arg | Tyr | Thr | Phe | Ala | Val | Leu | Ala | Arg | Met | | | |
| | 210 | | | | | 215 | | | | | 220 | | | | | | | |
| GCT | GAG | CCG | AGC | TTC | GGC | GGC | TTC | TGG | AGC | GCC | TGG | TCG | GAG | CCT | GTG | | | 720 |
| Ala | Glu | Pro | Ser | Phe | Gly | Gly | Phe | Trp | Ser | Ala | Trp | Ser | Glu | Pro | Val | | | |
| | 225 | | | | 230 | | | | | 235 | | | | | 240 | | | |
| TCG | CTG | CTG | ACG | CCT | AGC | GAC | CTG | GAC | CCC | CTC | ATC | CTG | ACG | CTC | TCC | | | 768 |
| Ser | Leu | Leu | Thr | Pro | Ser | Asp | Leu | Asp | Pro | Leu | Ile | Leu | Thr | Leu | Ser | | | |
| | | | | 245 | | | | | 250 | | | | | 255 | | | | |
| CTC | ATC | CTC | GTG | GTC | ATC | CTG | GTG | CTG | CTG | ACC | GTG | CTC | GCG | CTG | CTC | | | 816 |
| Leu | Ile | Leu | Val | Val | Ile | Leu | Val | Leu | Leu | Thr | Val | Leu | Ala | Leu | Leu | | | |
| | | | 260 | | | | | 265 | | | | | 270 | | | | | |
| TCC | CAC | CGC | CGG | GCT | CTG | AAG | CAG | AAG | ATC | TGG | CCT | GGC | ATC | CCG | AGC | | | 864 |
| Ser | His | Arg | Arg | Ala | Leu | Lys | Gln | Lys | Ile | Trp | Pro | Gly | Ile | Pro | Ser | | | |
| | | 275 | | | | | 280 | | | | | 285 | | | | | | |

| | |
|---|------|
| CCA GAG AGC GAG TTT GAA GGC CTC TTC ACC ACC CAC AAG GGT AAC TTC Pro Glu Ser Glu Phe Glu Gly Leu Phe Thr Thr His Lys Gly Asn Phe 290 295 300 | 912 |
| CAG CTG TGG CTG TAC CAG AAT GAT GGC TGC CTG TGG TGG AGC CCC TGC Gln Leu Trp Leu Tyr Gln Asn Asp Gly Cys Leu Trp Trp Ser Pro Cys 305 310 315 320 | 960 |
| ACC CCC TTC ACG GAG GAC CCA CCT GCT TCC CTG GAA GTC CTC TCA GAG Thr Pro Phe Thr Glu Asp Pro Pro Ala Ser Leu Glu Val Leu Ser Glu 325 330 335 | 1008 |
| CGC TGC TGG GGG ACG ATG CAG GCA GTG GAG CCG GGG ACA GAT GAT GAG Arg Cys Trp Gly Thr Met Gln Ala Val Glu Pro Gly Thr Asp Asp Glu 340 345 350 | 1056 |
| GGC CCC CTG CTG GAG CCA GTG GGC AGT GAG CAT GCC CAG GAT ACC TAT Gly Pro Leu Leu Glu Pro Val Gly Ser Glu His Ala Gln Asp Thr Tyr 355 360 365 | 1104 |
| CTG GTG CTG GAC AAA TGG TTG CTG CCC CGG AAC CCG CCC AGT GAG GAC Leu Val Leu Asp Lys Trp Leu Leu Pro Arg Asn Pro Pro Ser Glu Asp 370 375 380 | 1152 |
| CTC CCA GGG CCT GGT GGC AGT GTG GAC ATA GTG GCC ATG GAT GAA GGC Leu Pro Gly Pro Gly Gly Ser Val Asp Ile Val Ala Met Asp Glu Gly 385 390 395 400 | 1200 |
| TCA GAA GCA TCC TCC TGC TCA TCT GCT TTG GCC TCG AAG CCC AGC CCA Ser Glu Ala Ser Ser Cys Ser Ser Ala Leu Ala Ser Lys Pro Ser Pro 405 410 415 | 1248 |
| GAG GGA GCC TCT GCT GCC AGC TTT GAG TAC ACT ATC CTG GAC CCC AGC Glu Gly Ala Ser Ala Ala Ser Phe Glu Tyr Thr Ile Leu Asp Pro Ser 420 425 430 | 1296 |
| TCC CAG CTC TTG CGT CCA TGG ACA CTG TGC CCT GAG CTG CCC CCT ACC Ser Gln Leu Leu Arg Pro Trp Thr Leu Cys Pro Glu Leu Pro Pro Thr 435 440 445 | 1344 |
| CCA CCC CAC CTA AAG TAC CTG TAC CTT GTG GTA TCT GAC TCT GGC ATC Pro Pro His Leu Lys Tyr Leu Tyr Leu Val Val Ser Asp Ser Gly Ile 450 455 460 | 1392 |
| TCA ACT GAC TAC AGC TCA GGG GAC TCC CAG GGA GCC CAA GGG GGC TTA Ser Thr Asp Tyr Ser Ser Gly Asp Ser Gln Gly Ala Gln Gly Gly Leu 465 470 475 480 | 1440 |
| TCC GAT GGC CCC TAC TCC AAC CCT TAT GAG AAC AGC CTT ATC CCA GCC Ser Asp Gly Pro Tyr Ser Asn Pro Tyr Glu Asn Ser Leu Ile Pro Ala 485 490 495 | 1488 |
| GCT GAG CCT CTG CCC CCC AGC TAT GTG GCT TGC TCT TAG Ala Glu Pro Leu Pro Pro Ser Tyr Val Ala Cys Ser 500 505 | 1527 |

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 508 amino acids
- (B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Asp His Leu Gly Ala Ser Leu Trp Pro Gln Val Gly Ser Leu Cys
1 5 10 15
Leu Leu Leu Ala Gly Ala Ala Trp Ala Pro Pro Pro Asn Leu Pro Asp
20 25 30
Pro Lys Phe Glu Ser Lys Ala Ala Leu Leu Ala Ala Arg Gly Pro Glu
35 40 45
Glu Leu Leu Cys Phe Thr Glu Arg Leu Glu Asp Leu Val Cys Phe Trp
50 55 60
Glu Glu Ala Ala Ser Ala Gly Val Gly Pro Gly Asn Tyr Ser Phe Ser
65 70 75 80
Tyr Gln Leu Glu Asp Glu Pro Trp Lys Leu Cys Arg Leu His Gln Ala
85 90 95
Pro Thr Ala Arg Gly Ala Val Arg Phe Trp Cys Ser Leu Pro Thr Ala
100 105 110
Asp Thr Ser Ser Phe Val Pro Leu Glu Leu Arg Val Thr Ala Ala Ser
115 120 125
Gly Ala Pro Arg Tyr His Arg Val Ile His Ile Asn Glu Val Val Leu
130 135 140
Leu Asp Ala Pro Val Gly Leu Val Ala Arg Leu Ala Asp Glu Ser Gly
145 150 155 160
His Val Val Leu Arg Trp Leu Pro Pro Pro Glu Thr Pro Met Thr Ser
165 170 175
His Ile Arg Tyr Glu Val Asp Val Ser Ala Gly Asn Gly Ala Gly Ser
180 185 190
Val Gln Arg Val Glu Ile Leu Glu Gly Arg Thr Glu Cys Val Leu Ser
195 200 205
Asn Leu Arg Gly Arg Thr Arg Tyr Thr Phe Ala Val Leu Ala Arg Met
210 215 220
Ala Glu Pro Ser Phe Gly Gly Phe Trp Ser Ala Trp Ser Glu Pro Val
225 230 235 240
Ser Leu Leu Thr Pro Ser Asp Leu Asp Pro Leu Ile Leu Thr Leu Ser
245 250 255
Leu Ile Leu Val Val Ile Leu Val Leu Leu Thr Val Leu Ala Leu Leu
260 265 270
Ser His Arg Arg Ala Leu Lys Gln Lys Ile Trp Pro Gly Ile Pro Ser
275 280 285
Pro Glu Ser Glu Phe Glu Gly Leu Phe Thr Thr His Lys Gly Asn Phe
290 295 300

Gln Leu Trp Leu Tyr Gln Asn Asp Gly Cys Leu Trp Trp Ser Pro Cys
 305 310 315 320
 Thr Pro Phe Thr Glu Asp Pro Pro Ala Ser Leu Glu Val Leu Ser Glu
 325 330 335
 Arg Cys Trp Gly Thr Met Gln Ala Val Glu Pro Gly Thr Asp Asp Glu
 340 345 350
 Gly Pro Leu Leu Glu Pro Val Gly Ser Glu His Ala Gln Asp Thr Tyr
 355 360 365
 Leu Val Leu Asp Lys Trp Leu Leu Pro Arg Asn Pro Pro Ser Glu Asp
 370 375 380
 Leu Pro Gly Pro Gly Gly Ser Val Asp Ile Val Ala Met Asp Glu Gly
 385 390 395 400
 Ser Glu Ala Ser Ser Cys Ser Ser Ala Leu Ala Ser Lys Pro Ser Pro
 405 410 415
 Glu Gly Ala Ser Ala Ala Ser Phe Glu Tyr Thr Ile Leu Asp Pro Ser
 420 425 430
 Ser Gln Leu Leu Arg Pro Trp Thr Leu Cys Pro Glu Leu Pro Pro Thr
 435 440 445
 Pro Pro His Leu Lys Tyr Leu Tyr Leu Val Val Ser Asp Ser Gly Ile
 450 455 460
 Ser Thr Asp Tyr Ser Ser Gly Asp Ser Gln Gly Ala Gln Gly Gly Leu
 465 470 475 480
 Ser Asp Gly Pro Tyr Ser Asn Pro Tyr Glu Asn Ser Leu Ile Pro Ala
 485 490 495
 Ala Glu Pro Leu Pro Pro Ser Tyr Val Ala Cys Ser
 500 505